

GCTTGGAAAA CGCCTGCANT TGCNTGGCA TACNTGTTT TGGGTTNAAG GCTATGAACT 720
 5 GAATGAAAGG GCCCCNCTAC TGCNAAATT A NCCAAC TTGC TCCCCNAAAT TTGGTGCTAT 780
 AAAAANTGCC ACCNTTGATA TGCTTATNGG 810

(2) INFORMATION FOR SEQ ID NO: 24:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 765 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: cDNA

20 (vii) IMMEDIATE SOURCE:
 (B) CLONE: U-U103

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

GGCACGAGCT TGGCTGTAGT CTTCTTCTCA AGTAATCTTC GTCTTCTGA TTTGCTTGGT 60
 TGGTGGTCGG TTGCAGGGCG AAGGGATGGG GATGGGGAGG CCGAGCGGAG CTTGGTCGAC 120
 CCCGTGGTTG GTGGTGGTTC TTGTGCATTG GCTCCTCTGG GCCACCGAGA GGAGGGGAGG 180
 GGCGGTGGTG GAGGCCTCCC ATGTGGAGTT TGCATCCCTC CAATCTGTC CTGCCTCCGT 240
 CGTCGACAAC AGGCTGAGGA CTGGGTATCA CTTCCAGCCC CCGAGGAACG GGATCAACGA 300
 TCCAAATGGA CCCATGTACT TCAATGGCGT CTACCACCTC TTCTACCAAGT ACAACCCCAA 360
 TGGCTCCGTG TGGGGTAACA TCGTGTGGC CCACTCGGTG TCGACCGACC TCGTCAACTG 420
 40 GATAGCACTC GACCCGGCCA TCCGGCCAG CAAGCCATTG CACATCAACG GATGCTGGTC 480
 CGGCTCCGCC ACCGTCCCTCC CCGGCAACAG GCCTGCGATC TTCTACACCG GCATCNACCC 540
 CCANCANAAA CAACTGCANA ACNTNCNTN CCCAAGGATC TGTCCAACCT TACTCCCCNA 600
 45 NTGGGTCAAC CCCACTNCAA CCCCGTGTGATC CCCCTGGCGA CGCATCAACN CCACCCCTTC 660
 CNCNAACCCN AATACGGNTT GGCGCNGTCC CNGCACCCNC TGGAAACCCC TNGTNGGGAA 720
 50 CNANTTGAAN CNGAAGGGGA AAGGCNTTCT TTNCCGAACA GGGAT 765

(2) INFORMATION FOR SEQ ID NO: 25:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 774 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

60 (ii) MOLECULE TYPE: cDNA

65 (vii) IMMEDIATE SOURCE:
 (B) CLONE: U-U93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

70 GGCACGAGCG GAGAANGCAA TCTCGCTCTC TCTCTACTGC ATCGCGGCTC TCGTCCTCGA 60

	TTACTTGAGA TATGGCAGGA AAGGGCGAGG GGCCGGCGAT CGGGATCGAT CTCGGCACCA	120
	CGTACTCGTG CGTCGGGGTG TGGCAGCACG ACCGGGTGGA GATCATCGCC AACGATCAGG	180
5	GGAATCGTAC CACCCCCCTCC TATGTCGCCT TCACCGACTC CGAGCGCCTT ATCGGCGACG	240
	CTGCCAAGAA CCAGGTGCC ATGAACCCC TCAACACCGT CTTTGATGCA AAGCGTTAA	300
10	TTGGTAGGCG ATTCACTGAT TCATCTGTCC AGAGTGACAT CAAGCTCTGG CCTTTCAAGG	360
	TCATTCTGG TCCAGGTGAC AAGCCCATGA TTGTTGTCCA ATACAAAGGG GAGGATAAAC	420
	AGTTTGCAGC TGAAGATATT TCTTCCATGG TTTTGATAAA GATGAAAGAA ATTGCTGAAC	480
15	CTACCTGGGG TCTGTTGTCA AGAATGCCGT CCTCACTGTT CCCGCTTACT TCAATGACTC	540
	NCAACGCCA GCCACAAAGG ATGCTGGGT CATTGCTGGT CTCNATGTTA ATGANAATCA	600
20	TCAATGANCC CCCAGCACTG CTATTGCTTT ATGGCCTTGA CAAAANGCTA CTATTGTTGG	660
	TGAAAAAAAT TTCCTCATCT TCCATCTCCG GTGGGTGGCC TTTTGANTTC NCCTTCCTNA	720
	CCATCCAAGA AGGTTCTTT NAAGTCAAGG CCCTGCTGGT GANACCCANC TTGG	774

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 786 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
 (B) CLONE: U-U125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

	GGCACGAGCT AGTCTCGAGT TTTTTTTTT TTTTTTTAA AATTGAAATT AGATGCGATT	60
45	TCGAATAGCA AACATAGTTC AGGATAAACC AACAAACATTG TACCGAATTC GATAAGCTTA	120
	GGAAACTAAA TTGCGTAAAC GAAACACTTG CATGAAAGCC TATATAATAT AAGGCCGACT	180
50	AGGGACNAAA TAACTTAATC GACCTCTCG ATCTTGAC CAGCGCCGCT GCCACCAGCA	240
	GGAGGAGCAT CATCATCCAT ACCACCAGCC ATGTCAGCAC CTGCTCCCTG GTACATCTTG	300
	GCGATGATGG GATTGCATAT GCTCTCCAGC TCCTTCATCT TGTCATCGAA CTCGTCGGCT	360
55	TCTGCCAACT GGTTGCCATC GAGCATTGG ATGGCCTGCT CGATCGCATC CTCCGATCTT	420
	CTTCTTGTCA GCAGCAGCAA GCTTGGAGGC AATCTTGTG TCGTTAATGG TGTTCCCTCAT	480
60	GTTGTNAGCA TANNTTTCCA GANCATTCTT CCGATTCCAC CTTCCCTTTT ATGCTCCTCC	540
	ATCTTCCTGA CTTGTTACTT CTCCGCTTCC CTGCACCATT TTCTCAATCT CCTCCTTGCT	600
	GACCTACCTT GTCCTTGGTG AAGGTGATCT TGTTCTCTGT CCAGTGGTCT NTCNTCNGCA	660
65	GAAANATTCC AGAATACCAT TGGGGTTCCA AATGTTNCAA AACCAAACCC GGTGGATTCT	720
	TGAAGGAAAC CCCCCCTAA GGGCCCCAGG GTGGGAAATC CCCCCAAAAA ACCCCCCAAAT	780
70	TTTCCC	786

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23.

GGCACGAGCG AGTTTTTTT TTTTTTTTT TTTTTTTTT TTTTCACAAG GNAACCATAAG	60
ACATTACACC AAACATAGAT GTCAACAATA CATGCCAACG ATACCATTGC TTATTCCCTTC	120
AGACCTCCGA TAGGACTTCC ACGCACACCA ACAGAGAGAA CTAAGACAGC AAAGCAGCGG	180
ACACATACAG CCCAAAAGGG TNNGTGACCC CCGCGGAGGN GGAGCNCCAG GTGAAGGGTG	240
GATTCCCTCT GAATGTTGTA TTCTGNAGG GTGCGCCCGT CCTCNCNTTG NTTCCCNCT	300
NANATCNCCC NCTGNTGATC TGGTGGNAAT CCCCCCCTTG TCCTGTGATT CTTGCTCTTG	360
ACNTTTTCT CCCNTGTCNN ANCTCTCTNC CTNCTCTGGG TNNTGGGTCT TCCCTGTGTT	420
NANCNNCTN TTNNCNTATC ATCTTGTNCT CCNNCCNCCN CNCCTNTCNT TTCCTCNNNN	480
GGTNNA	486

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 791 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:
(B) CLONE: U-U116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GGCACGAGTG	ACAATGTCAA	GGCCAAGATT	CAGGATAAGG	AGGGCATTCC	CCCCGACCAAG	60
CAGAGGCTCA	TCTTGCCTGG	CAAGCAGCTC	GAGGATGGCC	GCACCTTGGC	TGATTACAAAC	120
ATCCAGAAGG	AGTCACCCCT	CCACCTTGTG	CTCCGCCCTCC	GTGGTGGCAT	GCACATCTTC	180
GTCAAGACTT	TGACTGGAA	GACCATCACC	CTTGAGGTGG	ANAGCTCGGA	CACCATCGAC	240
AATGTAAAGG	CCAAGATTCA	GGACAAGGGAG	GGTNTCCCC	CGGACCAGCA	AAGGCTCATC	300
TTTGCCTGGCA	AGCAGCTTGA	GGATGGCCGC	ACCCCTGGCAG	ATTACAACAT	TCAGAAGGAG	360
TCTACCCCTTC	ACCTTGTGCT	GANACTTAGG	GGTGGCATGC	ANATCTTGT	TAAGACNCTC	420
NCAGGGGAAG	ACCATTACCT	TGGAGGTGGA	NANCTCNGAC	ACGATTGATA	ATGTCNAGGC	480
AAAGATCCAN	GACAAGGANG	GGATTCCACC	GGATCAGCAN	ANGCTGATCT	TTGCTGGGAA	540